Applied Bioinformatics
July 11-18, 2020

For advanced graduate students, post-doctoral trainees, and researchers at all levels interested in incorporating bioinformatics into their research.

- Introduction to R and UNIX command line environments
- Command line tools such as FastQC, HISAT2 and HTSeq for dealing with RNA-seq data
- R Bioconductor tools like edgeR for analysis of differential gene expression
- Web-based tools such as Galaxy, UCSC Genome Browser and IGV for general genomics
- A survey of publicly available experimental data and gene annotation resources
- R packages for dimensional reduction, visualization, gene ontology and pathway analysis
- Introduction to cloud computing technology relevant to biomedical research
- An introduction to machine learning using CART models, random forests and support vector machines

For more information, visit: https://mdibl.org/course/applied-bioinformatics-2020/